Mutations in *TRAPPC11* are associated with a congenital disorder of glycosylation

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Summary

Congenital disorders of glycosylation (CDG) are a heterogeneous and rapidly growing group of diseases caused by abnormal glycosylation of proteins and/or lipids. Mutations in genes involved in the homeostasis of the endoplasmic reticulum (ER), the Golgi apparatus and the vesicular trafficking from the ER to the ER-Golgi intermediate compartment (ERGIC) have been found to be associated with CDG. Here, we report a patient with defects in both N- and O-glycosylation combined with a delayed vesicular transport in the Golgi apparatus due to mutations in *TRAPPC11*, a subunit of the TRAPPIII complex. TRAPPIII is implicated in the anterograde transport from the ER to the ERGIC as well as in the vesicle export from the Golgi apparatus. This report expands the spectrum of genetic alterations associated with CDG, providing new insights for the diagnosis and the understanding of the physiopathological mechanisms underlying glycosylation disorders.

Key words: CDG, TRAPPC11, Golgi, endoplasmic reticulum, vesicle trafficking

Congenital disorders of glycosylation (CDG) are a heterogeneous and rapidly growing group of diseases caused by abnormal glycosylation of proteins and/or lipids. Human CDG include mutations in genes involved in the homeostasis of the endoplasmic reticulum (ER) and the Golgi apparatus (GA) machinery. CDG patients show a highly heterogeneous clinical phenotype, usually presenting with symptoms during the neonatal period or infancy. The course of the disease is generally severe and the affected individuals show multiorgan involvement including central nervous system, muscle, liver, endocrine system, and coagulation abnormalities (Willett et al., 2013; Freeze et al., 2015). Although the altered glycoconjugates are diverse, the diagnosis of these individuals relies on the analysis of the glycosylation pattern of serum proteins. Serum transferrin (Tf) is the N-glycoprotein most widely used as a tool to detect N-glycosylation defects. In addition, apoCIII analysis, a mucin-type O-glycoprotein, is also useful to detect O-glycosylation defects. In fact, the aberrant glycosylation patterns of these proteins are reliable biomarkers that point to the potential molecular defects underlying these diseases: defects of N-glycan assembly (CDG-I), or N-glycan processing (CDG-II), or combined defects of N- and O-glycosylation.

Mutations in genes involved in the homeostasis of the ER and the GA as well as those implicated in the vesicle trafficking from the ER to the ER-Golgi intermediate compartment (ERGIC) have been found to be associated with CDGs. Indeed, mutations in genes encoding for proteins implicated in vesicular Golgi transport, such as the Conserved Oligomeric Golgi (COG) complex subunits [*COG1* (MIM# 606973), *COG2* (MIM# 606974), *COG3* (MIM# 606975), *COG4* (MIM# 606976), *COG5* (MIM# 606821), *COG6* (MIM# 606977), *COG7* (MIM# 606978), *COG8* (MIM# 606979)] were first described as a cause of N-glycosylation type II and O-glycosylation defects (Rosnoblet et al., 2013). In recent years, the implementation of next generation sequencing technologies has contributed decisively to the description of new CDGs and allowed the identification of new disease-

causing mutations in genes encoding for proteins implicated in the homeostasis of the Golgi apparatus [*ATP6V0A2* (MIM# 611716), *TMEM165* (MIM# 614726) and *TMEM199*, (MIM# 616815)].

Using whole exome sequencing we have identified a CDG patient with a defect in N- and O-glycosylation combined with a delayed ER to Golgi trafficking due to mutations in *TRAPPC11* (MIM# 614138), a subunit of the TRAPP III complex.

The patient was a boy from non-consanguineous parents. He was born prematurely at 33 weeks of gestation and weighed 1,550g. He presented with hypotonia and a malformation syndrome, with microcephaly, retrognatia, campydactilia, high foot arches (pes cavus) and abnormal facies. MRI showed brain atrophy. Later on, he developed cholestatic liver, recurrent thrombopenia, nephropathy with polyuria, alcalosis, hypernatremia and hypercalciuria, and also osteopathy with osteopenia and spontaneous fracture of the tibia. Neurophysiologic studies revealed motor and sensitive peripheral neuronopathy and an altered central auditory discrimination. He had recurrent infections, with moderate elevation of lactate. He died at 5 months of age.

Extensive metabolic studies were performed at 4 months of age. Metabolite analysis of plasma and urine included amino acids, organic acids, acyl carnitines, free fatty acids, very long chain fatty acids, polyunsaturated fatty acids, branched chain fatty acids and sterols. All of them showed normal results. Spleen necropsy showed hyperactivities of some lysosomal enzymes (ß-galactosidase, ß-hexosaminidase and ß-glucuronidase). However, ß-glucurocerebrosidase, galactocerebrosidase, ß-hexosaminidase, arylsulfatase and N-acetyl-α-galactosaminidase activities were normal in cultured fibroblasts.

Isoelectric focusing of serum Tf showed a glycosylation pattern compatible with CDG type II (Figure 1A). SELDI-TOF-MS analysis of plasma glycans revealed an abnormal percentage of N-glycan

structures compared to control values, with low biantennary and high monoantennary types of glycans (Figure 1A). These results were in agreement with those found through the analysis of serum Tf. Moreover, the apoCIII glycosylation pattern showed a clear increase of the non-sialylated forms (Figure 1A). These observations suggested a combined defect of both N- and O-glycosylation, pointing to a defect of the GA function. Therefore, alterations in the subunits of the COG complex (COG1-8) were analyzed by western blot and Sanger sequencing but no alterations were found in any of the COG subunits (data not shown). Consequently, we performed whole-exome sequencing of the patient and his healthy parents (Figure 1B). Since the biochemical phenotype showed a defect in both N- and O-glycosylation we filtered for variants of genes encoding for proteins involved in vesicle transport as well as in ER and GA functions. We used several filtering strategies and when a recessive inheritance pattern was postulated we identified two heterozygous missense mutations in *TRAPPC11* (transport protein particle complex 11). These mutations (c.1141C>G and c.3310A>G) were predicted to change proline 381 to alanine (p.Pro381Ala) and threonine 1104 to alanine (p.Thr1104Ala), respectively (Figure 1B-C) (GenBank accession number NM_021942.5, nucleotide numbering uses +1 as the A of the ATG translation initiation codon in the reference sequence, with the initiation codon as codon 1). The c.1141C>G mutation was not annotated in the Exome Aggregation Consortium (ExAC) database (LSDB database: http://databases.lovd.nl/shared/variants/0000132350). Interestingly, the c.3310A>G substitution (rs78663235) has already been reported in the ExAC database with a global allele frequency of 0.0015, but no homozygous individuals for this change have been reported in the European population. Compound heterozygosity was corroborated by the carrier status of the father (c.[3310A>G]+[=]) and the mother (c.[1141C>G]+[=]). Results were confirmed by Sanger sequencing. *TRAPPC11* encodes for a large protein of 1133 amino acids with two conserved

functional regions: the foie gras and gryzum domains (Figure 1C). TRAPPC11 has been described to be involved in the assembly and integrity of the TRAPP III complex, which is implicated in the anterograde vesicular membrane transport from the ER to the ERGIC as well as in vesicle mediated export from the Golgi in mammals (Kim et al., 2006; Scrivens et al., 2011; Brunet et al., 2014). The two missense variants identified in our patient correspond to highly conserved amino acids in higher eukaryotes, one of them within the foie gras domain (Figure 1C and Supplementary Figure 1). The fact that the TRAPPC11 protein levels in fibroblasts of the patient were similar to those seen in control cells suggest that these mutations do not compromise the stability of the protein but likely its function in the whole complex (Figure 1D). Moreover, the subcellular localization of TRAPPC11 was not affected by the mutations reported in this patient, since the protein properly localizes in the GA, as expected (Supplementary Figure 2).

Previous studies identified mutations in *TRAPPC11* in three families with a clinical phenotype of muscular dystrophy and myopathy with movement disorders and intellectual disability (Bögershausen et al., 2013), in another patient with congenital muscular dystrophy with fatty liver and infantile-onset cataracts (Liang et al., 2015) and recently in four patients from two unrelated families with triple A syndrome (MIM# 231550) (Kohler et al., 2016). However, none of these patients were identified to be associated with an abnormal Tf or ApoCIII profile, nor with a CDG syndrome. Immunofluorescence studies using antibodies against *cis* and *trans*-Golgi markers demonstrated a severe fragmentation of the GA in one of the previous reports (Bögershausen et al., 2013). Intriguingly, the morphology of the GA was normal in fibroblasts from our patient, as no significant differences were found in the degree of Golgi compaction compared to control cells (Figure 1A). As TRAPPC11 is known to be involved in ER to Golgi vesicular trafficking, we therefore tested whether this pathway was affected by *TRAPPC11* mutations. Thus, cells were treated with brefeldin A (BFA), an inhibitor of the ER-Golgi

anterograde transport (Jackson et al., 2000). Upon BFA treatment both, patient and control fibroblasts showed the complete disassembly of the GA (Figure 1A). Interestingly, after the removal of BFA, a significant delay in the reassembly of the GA was observed in patient fibroblasts. These results revealed a defect in the anterograde vesicular transport in the TRAPPC11 patient reported here (Figure 1A). In addition, the functionality of the retrograde Golgi vesicle transport was also assessed in our patient but no abnormalities were observed (data not shown). These results are in agreement with the vesicular stomatitis virus (VSV-G) trafficking defect observed in the patients reported by Bögershausen et al (2013).

Previous studies in mammalian cellular models have demonstrated that the presence of TRAPPC11 is critical to keep the integrity of the TRAPP III complex, as its total depletion resulted in strong fragmentation of both, the Golgi apparatus and the ERGIC (Scrivens et al., 2011. However, in our patient an alteration in the GA dynamics was only detected upon BFA treatment. We hypothesise that the normal expression levels and the correct subcellular localization of the mutant TRAPPC11 protein of our patient may be sufficient to maintain, at least partially, the integrity of the TRAPP III complex and, subsequently, the structure of the Golgi apparatus regardless of the evident ER-Golgi anterograde transport defect (Figure 1D, Supplementary Figure 2A). However, the question whether the slight TRAPPC11 alteration resulted in such a severe clinical phenotype remains unanswered.

The main biochemical feature of the TRAPPC11 patient reported here is the abnormal N and O-glycosylation pattern detected in plasma Tf and apoCIII proteins (Figure 1A). This finding is novel and provides a reliable biochemical marker for the diagnosis of this disorder. Moreover, our observations are supported by a recently published study using a zebrafish model carrying a mutation in the TRAPPC11 foie gras domain (DeRossi et al., 2016). In that work, the authors demonstrated that lipid-linked oligosaccharides were decreased in the TRAPPC11 mutant animals and hypothesised that

TRAPPC11 deficiency causes a dysfunction in the synthesis of dolichol, a substrate required for the protein N-glycosylation, and the induction of the unfolded-protein response (UPR). Moreover, HeLa cells treated with siRNA against *TRAPPC11* showed an abnormal accumulation of the non-glycosylated form of the signal sequence receptor α (SSR1), a protein marker with two glycosylation sites not processed in the GA (DeRossi et al., 2016). These results were unexpected as they could not be explained by the already known role of TRAPPC11 in trafficking. Interestingly, the downregulation of other TRAPP III subunits showed no defects in protein glycosylation. In fact, it is known that several TRAPP III complex subunits have additional functions other than vesicle trafficking (Gedeon et al., 1999; Milev et al., 2015). Thus, in addition to the role in maintaining TRAPP III complex integrity, TRAPPC11 may also be involved in the regulation of N-linked glycosylation and, as a consequence, protein glycosylation might be altered in patients with *TRAPPC11* mutations. To this effect, two recent reports showed that LAMP1 protein could be either hypo- or hyper- glysosylated in TRAPPC11 patients. These apparently controversial results could reflect, in fact, a membrane trafficking defect caused by TRAPC11 deficiency.

The patient reported here showed a constitutive activation of the UPR, mimicking the observations made in TRAPPC11-deficient cellular and animal models (Figure 2) (DeRossi et al., 2016). Moreover, our results suggested that the N-glycosylation defects observed in our patient cannot only be attributed to a dysfunction in the dolichol synthesis pathway, as previously hypothesised (DeRossi et al., 2016), since dolichol levels in liver necropsy from our patient were similar to those found in age matched controls (Supplementary Figure 3). Therefore, the strong UPR activation observed in our patient suggests that the glycosylation defects may result in the accumulation of unfolded/misfolded proteins in the ER regardless of the dolichol levels. Altogether these observations point to a

widespread role of TRAPPC11 in the molecular and cellular pathways involved in protein glycosylation and Golgi vesicular transport.

In summary, this report expands the spectrum of genetic alterations associated with CDG, providing new insights into the diagnosis as well as for the understanding of the physiopathological mechanisms underlying vesicle trafficking defects and glycosylation disorders. We highlight the importance of an accurate biochemical characterization to direct the genetic data analysis when using next generation sequencing tools. Our study demonstrates that TRAPPC11 deficiency could lead to a disorder targeting the GA function which might be readily identified by routine screening for abnormal glycosylation patterns of plasma proteins.

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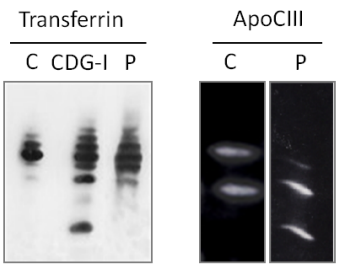
Potential conflicts of Interest: The authors have no conflicts of interest to disclose.

Ethics: All the procedures were approved by the ethics committee of the Hospital Clínic, Barcelona. All procedures followed were in accordance with the ethical standards of the responsible committee on human experimentation (Hospital Clínic de Barcelona) and with the Helsinki Declaration of 1975, as revised in 2000.

FIGURE LEGENDS

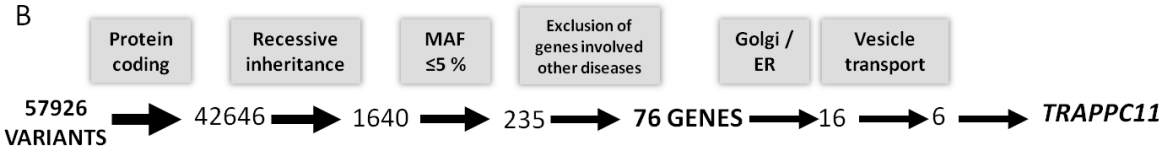
Figure 1. Identification of *TRAPPC11* mutations in a patient with defects in N- and O-glycosylation. (A) Analysis of plasma glycans from the TRAPPC11 patient by SELDI-TOF-MS in negative ion mode (left panel) together with Transferrin and Apo CIII glycosylation patterns (right panel) of a control individual (C), a CDG type I patient (CDG-I) and the TRAPPC11 patient (P). SELDI-TOF-MS showed an altered percentage of N-glycan structures compared to control values. The major abnormal species corresponds to biantennary N-linked glycan that lacks a single sialic acid (SA) residue and a single galactose (Gal) residue. Relative amounts are presented as a percentage of the total identified N-linked glycan structures compared to control values. n.d.: not detectable; SA: sialic acid; Gal: galactose; GlcNac: N-Acetylglucosamine. (B) Exome data analysis and filtering steps leading to the identification of *TRAPPC11* as a putative genetic cause of the disease. (C) Human TRAPPC11 protein scheme showing the position of the identified mutations. (D) Western blot analysis of TRAPPC11 in patient fibroblasts (P) and in a control individual (C). SDHA was used as loading control.

A



		Control	Patient
Biantenanary-SA-Gal-GlcNac		n.d.	5%
Biantennary-SA-Gal		n.d.	9%
Biantennary-SA		11%	21%
Biantennary		50%	36%
Triantennary		6%	n.d.

B



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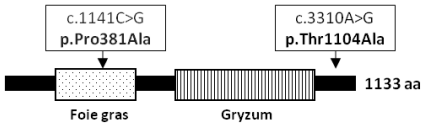

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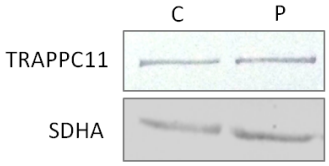

Figure 2. ER-to-Golgi anterograde membrane flow is defective in the TRAPPC11 patient. (A) Fibroblasts from the TRAPPC11 patient and from a control individual were treated with brefaldin A (BFA) for 15 min to block ER-Golgi anterograde transport. (B) After BFA removal, the percentage of cells with assembled Golgi apparatus together with the (C) Golgi compactation index (calculated as $4\pi*\Sigma(\text{areas})/\Sigma(\text{perimeter})^2$) were analyzed at different time points, using the Fiji image processing package (Schindelin et al., 2012). Antibody against GM130 was used to stain the Golgi apparatus. (D) Fibroblasts from TRAPPC11 patient and from a control individual were analyzed by qPCR for expression of four UPR (unfolded protein response) effectors and target genes using the comparative Ct method. *GAPDH* gene was used as an internal control. Results are expressed in relative units (RU),* $p<0.05$.